OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: May 28, 2005, 23:00:05 ; Search time 4174.5 Seconds
                                        (without alignments)
                                        11934.968 Million cell updates/sec

Title: US-09-778-516C-2
Perfect score: 8115
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Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0
Searched: 5700845 seqs, 306977957 residues

Total number of hits satisfying chosen parameters: 11401690

Post-processing: Minimum Match 0%
                 Maximum Match 100%
Maximum DB seq length: 200000000
Minimum DB seq length: 0
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB ID	Description
1	8115	100.0	8115	9	US-09-778-516A-2	Sequence 2, Appli
2	5812.4	71.6	8115	9	US-09-778-516A-1	Sequence 1, Appli
c 3	2115	26.1	8115	9	US-09-778-516A-1	Sequence 1, Appli
4	1567.4	19.3	5155	19	US-10-492-403A-9	Sequence 9, Appli
5	1507	18.6	5175	17	US-10-285-874-14	Sequence 14, Appl
6	1502.4	18.5	5178	17	US-10-285-874-13	Sequence 13, Appl
7	1264.2	15.6	3982	17	US-10-387-252-3	Sequence 3, Appli
8	1223.6	15.1	5308	10	US-09-826-115-15	Sequence 15, Appl
9	1222.6	15.1	5334	10	US-09-826-115-17	Sequence 17, Appl
10	1215.6	15.0	5283	10	US-09-826-115-19	Sequence 19, Appl
11	1215.4	15.0	5271	10	US-09-826-115-23	Sequence 23, Appl

12	1215.4	15.0	5304	10	US-09-826-115-21	Sequence 21, Appl
13	1169.2	14.4	4059	18	US-10-655-702-1	Sequence 1, Appli
14	1152.4	14.2	5314	16	US-10-331-329-27	Sequence 27, Appl
15	1151.6	14.1	5382	16	US-10-331-329-21	Sequence 21, Appl
16	1148.2	14.1	14455	9	US-09-847-101B-15	Sequence 15, Appl
c 17	1148.2	14.1	14455	10	US-09-482-682-15	Sequence 15, Appl
c 18	1141.8	14.1	4644	16	US-10-331-329-19	Sequence 19, Appl
19	1109.8	13.7	5247	16	US-10-331-329-20	Sequence 20, Appl
20	1082	13.3	5446	9	US-09-844-645-3	Sequence 3, Appli
21	1082	13.3	5446	9	US-09-559-874-5	Sequence 5, Appli
22	1082	13.3	5446	17	US-10-371-116A-1	Sequence 1, Appli
23	1068	13.2	8705	15	US-10-291-230-14	Sequence 14, Appl
24	1068	13.2	8705	15	US-10-291-249-14	Sequence 14, Appl
25	1068	13.2	8705	17	US-10-273-678-16	Sequence 16, Appl
26	1058.4	13.0	4622	9	US-09-846-091-11	Sequence 11, Appl
27	1058.4	13.0	6050	15	US-09-491-974-4	Sequence 4, Appli
28	1058.4	13.0	6050	17	US-10-394-388A-4	Sequence 4, Appli
29	1056.8	13.0	6001	9	US-09-491-974-3	Sequence 3, Appli
30	1056.6	13.0	8001	15	US-10-394-388A-3	Sequence 3, Appli
31	1053.6	13.0	7807	17	US-10-394-388A-7	Sequence 7, Appli
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33	1052	13.0	13464	17	US-10-394-388A-9	Sequence 9, Appli
34	1036.2	12.8	3796	13	US-10-127-391-32	Sequence 32, Appl
35	1036.2	12.8	3796	13	US-10-241-332-32	Sequence 32, Appl
36	988	12.2	4597	15	US-10-277-184-3	Sequence 3, Appli
37	983	12.1	4058	19	US-10-811-028A-5	Sequence 5, Appli
38	983	12.1	4187	19	US-10-811-028A-6	Sequence 6, Appli
39	983	12.1	4293	19	US-10-811-028A-2	Sequence 2, Appli
40	983	12.1	4332	19	US-10-811-028A-1	Sequence 1, Appli
41	983	12.1	5753	19	US-10-811-028A-3	Sequence 3, Appli
42	983	12.1	5760	19	US-10-811-028A-4	Sequence 4, Appli
43	981.8	12.1	6565	14	US-10-267-117-1	Sequence 1, Appli
44	981.8	12.1	6565	14	US-10-340-112-1	Sequence 1, Appli
45	981.8	12.1	6981	14	US-10-267-117-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-778-516A-2
Sequence 2, Application US/09778516A
Patent No. US2020102722A1
; GENERAL INFORMATION:
; APPLICANT: Lo, Wei-Yu
; APPLICANT: Lo, Ming Ching
; APPLICANT: Liau, Pei-Ru
; TITLE OF INVENTION: LAC SHUTTLE VECTORS
; FILE REFERENCE: 12875-002001
; CURRENT APPLICATION NUMBER: US/09/778,516A
; CURRENT FILING DATE: 2007-02-07
; PRIOR APPLICATION NUMBER: TW 89110235
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 8115
;   TYPE: DNA
;   ORGANISM: Lactobacillus plantarum
US-09-778-516A-2

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OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: May 28, 2005, 19:59:45 ; Search time 1161 Seconds
                                      (without alignments)
                                      11437.025 Million cell updates/sec

Title: US-09-778-516C-2
Perfect score: 8115
Sequence: 1 gatgtgacgggccagatatac..........gcgtgtcgctagcgacggtc 8115

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
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4	1152.4	14.2	5314	3	US-09-479-122-27	Sequence 27, Appli
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6	1152.4	14.2	5314	3	US-09-481-355-27	Sequence 27, Appli
7	1152.4	14.2	5314	3	US-09-484-282-27	Sequence 27, Appli
8	1152.4	14.2	5314	3	US-09-455-659A-27	Sequence 27, Appli
9	1152.4	14.2	5314	3	US-09-484-996-27	Sequence 27, Appli
10	1152.4	14.2	5314	3	US-09-479-123-27	Sequence 27, Appli
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23	1141.8	14.1	4644	4	US-09-455-659A-19	Sequence 19, Appl
24	1141.8	14.1	4644	4	US-09-484-996-19	Sequence 19, Appl
25	1141.8	14.1	4644	4	US-09-479-123-19	Sequence 19, Appl
26	1141.8	14.1	4644	4	US-09-484-317A-19	Sequence 19, Appl
27	1109.8	13.7	5247	3	US-09-479-122-20	Sequence 20, Appl
28	1109.8	13.7	5247	4	US-09-484-997-20	Sequence 20, Appl
29	1109.8	13.7	5247	4	US-09-481-355-20	Sequence 20, Appl
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31	1109.8	13.7	5247	4	US-09-455-659A-20	Sequence 20, Appl
32	1109.8	13.7	5247	4	US-09-484-996-20	Sequence 20, Appl
33	1109.8	13.7	5247	4	US-09-479-123-20	Sequence 20, Appl
34	1109.8	13.7	5247	4	US-09-484-317A-20	Sequence 20, Appl
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36	1068.6	13.2	4026	3	US-09-315-113-19	Sequence 19, Appl
37	1068	13.2	8705	3	US-09-647-344A-14	Sequence 14, Appl
38	1053.6	13.0	4326	3	US-09-760-615-7	Sequence 7, Appl
39	1036.2	12.8	3796	4	US-09-470-661A-32	Sequence 32, Appl
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41	985.2	12.1	5128	4	US-09-721-480-2	Sequence 2, Appli
42	985.2	12.1	5459	4	US-09-721-480-4	Sequence 4, Appli
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44	981.8	12.1	6253	3	US-08-893-327-15	Sequence 15, Appl
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ALIGNMENTS

RESULT 1
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Sequence 5, Application US/08801092
Patent No. 6074850
; GENERAL INFORMATION:
; APPLICANT: Antelman, Douglas
; APPLICANT: Gregory, Richard J.
; APPLICANT: Wils, Kenneth N.
; TITLE OF INVENTION: Tissue Specific Expression of
; TITLE OF INVENTION: Retinoblastoma Protein
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,092
; FILING DATE: 14-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/751,517
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 016930-001020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 703-576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3853 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 209..250
; FEATURE:
; NAME/KEY: CDS

OM nucleic - nucleic search, using sw model

Run on: May 28, 2005, 23:00:05 ; Search time 4174.5 Seconds
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6	1502.4	18.5	5178	17	US-10-285-874-13	Sequence 13, Appl
7	1264.2	15.6	3982	17	US-10-387-252-3	Sequence 3, Appli
8	1223.6	15.1	5308	10	US-09-826-115-15	Sequence 15, Appl
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23	1068	13.2	8705	15	US-10-291-230-14	Sequence 14, Appl
24	1068	13.2	8705	15	US-10-291-249-14	Sequence 14, Appl
25	1068	13.2	8705	17	US-10-273-678-16	Sequence 16, Appl
26	1058.4	13.0	4622	9	US-09-491-974-11	Sequence 11, Appl
27	1058.4	13.0	4644	9	US-09-491-974-4	Sequence 4, Appli
28	1058.4	13.0	6050	17	US-10-291-249-13	Sequence 13, Appl
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31	1053.6	13.0	7807	17	US-10-394-388A-7	Sequence 7, Appli
32	1052	13.0	7913	17	US-10-394-388A-8	Sequence 8, Appli
33	1052	13.0	13464	17	US-10-394-388A-9	Sequence 9, Appli
34	1036.2	12.8	3796	15	US-10-127-391-32	Sequence 32, Appl
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37	983	12.1	4058	19	US-10-811-028A-5	Sequence 5, Appli
38	983	12.1	4187	19	US-10-811-028A-6	Sequence 6, Appli
39	983	12.1	4293	19	US-10-811-028A-2	Sequence 2, Appli
40	983	12.1	4332	19	US-10-811-028A-2	Sequence 2, Appli
41	983	12.1	5753	19	US-10-811-028A-3	Sequence 3, Appli
42	983	12.1	5760	19	US-10-811-028A-4	Sequence 4, Appli
43	981.8	12.1	6565	14	US-10-267-117-1	Sequence 1, Appli
44	981.8	12.1	6565	14	US-10-340-112-1	Sequence 1, Appli
45	981.8	12.1	6981	14	US-10-267-117-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-778-516A-1
Sequence 1, Application US/09778516A
Patent No. US2002010272722A1
GENERAL INFORMATION:
; APPLICANT: Lo, Wei-Yu
; APPLICANT: Lo, Ming Ching
; APPLICANT: Liau, Pei-Ru
; TITLE OF INVENTION: LAC SHUTTLE VECTORS
; FILE REFERENCE: 12875-002001
; CURRENT APPLICATION NUMBER: US/09/778,516A
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: TW 89110235
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 8115
; TYPE: DNA
; ORGANISM: Lactobacillus plantarum
US-09-778-516A-1

Query Match   100.0%; Score 8115; DB 9; Length 8115;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 8115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GATGTACGGGCCAGATATACGCGTTGACATTGATTATTGACTAGTTATTAATAGTAATCA 60

Qy   61 ATTACGGGGGGTTCATTAGTTCATTAGCCCCATTATATGGAGGAGTTCCGCGTTACGGGTA 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATTACGGGGGGTTCATTAGTTCATTAGCCCCATTATATGGAGGAGTTCCGCGTTACGGGTA 120

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                          GenCore version 5.1.6
                          Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          May 28, 2005, 19:59:45 ; Search time 1161 Seconds
                                           (without alignments)
                                           11437.025 Million cell updates/sec

Title:           US-09-778-516C-1
Perfect score:   8115
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Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters:          2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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                 Pred. No. is the number of results predicted by chance to have a
                 score greater than or equal to the score of the result being printed,
                 and is derived by analysis of the total score distribution.

                                          SUMMARIES

Result                    %     Query
No.      Score       Match  Length  DB    ID                         Description
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 1      1240.4       15.3    3853   3     US-08-801-092-5            Sequence 5, Appli
 2      1240.4       15.3    3853   3     US-09-315-113-5            Sequence 5, Appli
 3      1152.4       14.2    5314   3     US-09-479-122-27           Sequence 27, Appl
 4      1152.4       14.2    5314   4     US-09-484-997-27           Sequence 27, Appl
 5      1152.4       14.2    5314   4     US-09-481-355-27           Sequence 27, Appl
 6      1152.4       14.2    5314   4     US-09-481-282-27           Sequence 27, Appl
 7      1152.4       14.2    5314   4     US-09-455-659A-27          Sequence 27, Appl
 8      1152.4       14.2    5314   4     US-09-484-996-27           Sequence 27, Appl
 9      1152.4       14.2    5314   4     US-09-479-123-27           Sequence 27, Appl
10      1152.4       14.2    5314   3     US-09-484-317A-27          Sequence 27, Appl
11      1151.6       14.2    5382   3     US-09-479-122-21           Sequence 21, Appl
12      1151.6       14.2    5382   4     US-09-484-997-21           Sequence 21, Appl
13      1151.6       14.2    5382   4     US-09-481-355-21           Sequence 21, Appl
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15      1151.6       14.2    5382   4     US-09-455-659A-21          Sequence 21, Appl
16      1151.6       14.2    5382   4     US-09-484-996-21           Sequence 21, Appl
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18      1151.6       14.2    5382   3     US-09-484-317A-21          Sequence 21, Appl
19      1141.8       14.1    4644   3     US-09-479-122-19           Sequence 19, Appl
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27      1109.8       13.7    5247   3     US-09-479-122-20           Sequence 20, Appl
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35      1068.6       13.2    4026   4     US-08-801-092-19           Sequence 19, Appl
36      1068.6       13.2    4026   3     US-09-315-113-19           Sequence 19, Appl
37      1068        13.2    8705   3     US-09-647-344A-14          Sequence 14, Appl
38      1053.6       13.0    4326   3     US-08-760-615-7            Sequence 7, Appli
39      1036.2       12.8    3796   4     US-09-721-480-1            Sequence 1, Appli
40      985.2        12.1    4276   4     US-09-721-480-1            Sequence 1, Appli
41      985.2        12.1    5128   4     US-09-721-480-2            Sequence 2, Appli
42      985.2        12.1    5459   4     US-09-721-480-4            Sequence 4, Appli
43      985.2        12.1    5882   4     US-09-721-480-6            Sequence 6, Appli
44      981.8        12.1    6253   3     US-08-893-327-15           Sequence 15, Appl
45      981.8        12.1    6280   3     US-08-893-327-17           Sequence 17, Appl


                                          ALIGNMENTS

RESULT 1
US-08-801-092-5
Sequence 5, Application US/08801092
Patent No. 6074850
GENERAL INFORMATION:
  APPLICANT: Antelman, Douglas
  APPLICANT: Gregory, Richard J.
  APPLICANT: Wils, Kenneth N.
  TITLE OF INVENTION: Tissue Specific Expression of
  TITLE OF INVENTION: Retinoblastoma Protein
  NUMBER OF SEQUENCES: 46
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
    STREET: Two Embarcadero Center, 8th Floor
    CITY: San Francisco
    STATE: CA
    COUNTRY: USA
    ZIP: 94111
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/801,092
    FILING DATE: 14-FEB-1997
    CLASSIFICATION: 514
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/751,517
    FILING DATE: 15-NOV-1996
    CLASSIFICATION: 514
  ATTORNEY/AGENT INFORMATION:
    NAME: Fitts, Renee A.
    REGISTRATION NUMBER: 35,136
    REFERENCE/DOCKET NUMBER: 016930-001020
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 415-576-0200
    TELEFAX: 703-576-0300
INFORMATION FOR SEQ ID NO: 5:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 3853 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: DNA (genomic)
  FEATURE:
    NAME/KEY: CDS
    LOCATION: 209..250
  FEATURE:
    NAME/KEY: CDS
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